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Incorporating population dynamics into household models of infectious disease transmission

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ABSTRACT

Most household models of disease transmission assume static household distributions. Although this is a reasonable simplification for assessing vaccination strategies at a single point in time or over the course of an outbreak, it has considerable drawbacks for assessing long term vaccination policies or for predicting future changes in immunity. We demonstrate that household models that include births, deaths and movement between households can show dramatically different patterns of infection and immunity to static population models. When immunity is assumed to be life-long, the pattern of births by household size is the key driver of infection, suggesting that the influx of susceptibles has most impact on infection risk in the household. In a comparison of 12 countries, we show that both the crude birth rate and the mean household size affect the risk of infection in households.

Introduction

The household has long been known to play an important role in transmission of infection (Hope-Simpson, 1952; Ounsted, 1950). Analyses of social mixing patterns show that contacts with household members are more likely to involve physical contact, last longer and occur more frequently (Hens et al., 2009). Evidence of heightened risk of infection among family members of an infected case has been demonstrated for seasonal and pandemic influenza (Cauchemez et al., 2009; Viboud et al., 2004), for pneumococcal carriage (Melegaro et al., 2004), and for childhood infections (Hope-Simpson, 1952; Crowcroft and Pebody, 2006). In recognition of this, disease control measures are often directed at household members. Such interventions range from household-based interventions to slow the spread of pandemic influenza (Wu et al., 2006), through to "cocoon" vaccination of parents of newborns to protect infants from infection with pertussis (Coudeville et al., 2007).

Although immunisation has greatly reduced the burden of infection, elimination remains an elusive goal for most vaccine preventable diseases (Mulholland, 1995). Prior to the introduction of mass vaccination, the mean age of infection for diseases such as measles and pertussis was around 5 years old (Edmunds et al., 2000; Anderson and May, 1982). While vaccination has reduced the incidence of infection of these diseases, it has also led to changes in the patterns of immunity and infection, such as the rise in pertussis cases in adolescents and young adults (Crowcroft and Pebody, 2006) and the decline in maternally derived protection against measles in infants (McLean, 1995). Demographic trends in developed countries show a predictable pattern of population ageing and declining household sizes (Jennings et al., 1999). Such trends have implications for population immunity, as smaller households lead to reduced opportunities for boosting of immunity through household transmission. These changes may lead to unexpectedly rapid waning of immunity (McVernon et al., 2004; Glass and Grenfell, 2004) and more severe disease outcomes (Aguas et al., 2006). The complexity of the relationship between infection and immunity make mathematical models an ideal tool for investigating optimal vaccine strategies. Models of disease spread in households allow us to characterise vulnerable household types, compare vaccine delivery strategies, and predict the risk of disease resurgence.

Mathematical models used to assess disease interventions such as vaccination are often based around households (Becker and Dietz, 1995; Hall and Becker, 1996; House and Keeling, 2008, 2009; Dodd and Ferguson, 2007; Ball and Lyne, 2002; Ball et al., 2007). They adopt either theoretical or empirical distributions for household sizes, and identify the optimal use of vaccines to raise or maintain population immunity. Although some age-structured models incorporate realistic patterns of births (Hethcote, 1997), most household models assume that the population is static – that is, that individuals stay in the same household throughout the period of study, and that household sizes do not change. This simplification works well for assessing strategies at a single point in

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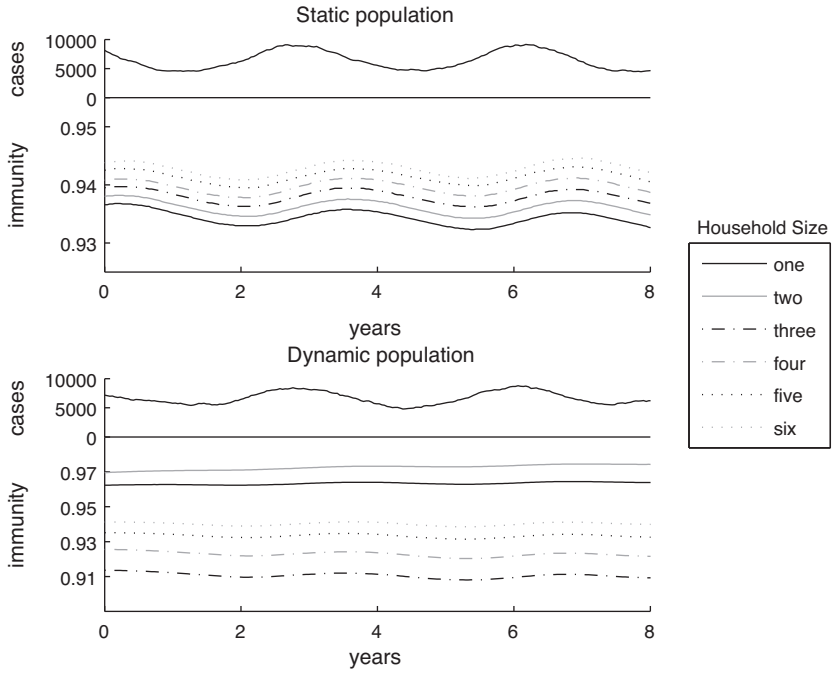

Fig. 1. Comparison of a simple static model of household transmission, and a dynamic model including births, deaths and movement between households. Each pair of graphs shows new cases over time and the fraction of individuals in households of sizes 1–6 that are immune. Note the different vertical axis scales comparing immunity between two models.

time, or over the timescale of an outbreak, but is clearly unsatisfactory for considering the medium to long term impact of vaccination programs.

In this paper, we present results using a simple model of births, deaths and movement between households incorporated into a household model of disease transmission. Using parameter values consistent with measles, we explore the impact of demographic transitions on the distribution of immunity in the population, by household size. We compare a dynamic population to a static population and identify the parameters that have most impact on immunity. We then compare the results across a range of countries with differing birth rates and mean household sizes, and consider the effect that these parameters have on risk of infection.

Methods

We adopt a stochastic, generation-based household model of disease transmission, and overlay a simple, flexible model of births, deaths, and movement between households. The different components of the model and the data used to parameterise it are described below.

Disease transmission model

We use a stochastic model of disease transmission in a population of 19 million individuals across 7.4 million households of sizes 1–6. Household sizes and compositions are based on data from the 2001 Australian census (as described elsewhere (Becker et al., 2005)). Owing to computational limitations, and a desire to keep the model as simple as possible, age structure is not included. The model progresses in generations, so that the state of the system at any time includes the number of households with n_I infected individuals, n_S susceptible individuals and n_R recovered (immune) individuals for every plausible choice of n_I, n_S, and n_R. In each generation of transmission, an individual has a probability of being infected that depends on the force of infection acting on them from outside the household and the number of infected individuals inside their household. When plotting the output of the model against calendar time, we have assumed a generation interval of 14 days, which is roughly appropriate to measles (Anderson and May, 1982).

Within the household, disease spreads according to a Reed–Frost model (Bailey, 1975), where θ is the Reed–Frost parameter giving the probability of escaping infection from an infected household member. Between household transmission is calibrated by the parameter μ, which translates to an escape probability $q_{out} = 1 - \mu I/N$ per generation, where I is the current number of infected individuals, and N is the total population size. We choose parameters $\mu = 15$, and $\theta = 0.4$ to give high transmission rates that are characteristic of measles (Anderson and May, 1982). Using these values, a randomly selected infected individual in a fully susceptible population will infect around 17 individuals, and 80–100% of their household will be infected. The default Reed–Frost model assumes that within-household transmission rates do not vary with household size. We tested the impact of an alternative model of household transmission in which transmission rates decline with household size (see online Appendix B). Under the default 'measles-like' parameters, the two models showed very similar patterns of immunity. We also simulated an alternative moderately transmissible disease with $\mu = 5$, and $\theta = 0.6$ (corresponding to around 6.5 individuals infected by a single case, and 65–80% of the household infected when the population is fully susceptible), and a low-transmission 'influenza-like' disease with $\mu = 1.2$, and $\theta = 0.8$ (corresponding to around 1.8 individuals infected by a single case, and 40–55% of the household infected when the population is fully susceptible). Although population immunity varies with these transmission patterns, the pattern of immunity by household size is consistent across all three scenarios under both household transmission model. More details are provided in Appendix B.

As shown in Fig. 1, the parameters $\mu = 15$, and $\theta = 0.4$ produce approximately biennial cycles and high levels of immunity typical of measles at moderate birth rates (Earn et al., 2000). The model does not include a seasonal forcing term; rather, the cycles are a consequence of the discrete-time formulation. These cycles persist

in both the static and dynamic models over extended simulation. As discussed elsewhere (Glass et al., 2003), discrete-time models can have different bifurcation structure from continuous-time models, and a closer approximation to the continuous-time model can be achieved by adjusting the transmission term to the form $\mu SI^{\alpha}/N$, where α is slightly less than one. In this model, this change dampens the persistent cycles seen in Fig. 1, but otherwise does not change the underlying patterns of infection and immunity by household size. As it is this mean equilibrium behaviour that interests us here, we have retained the standard transmission term, but note that the cyclical behaviour is largely an artifact of the generation-based formulation. In the simulations presented here, we run the model for a period of 500 generations to ensure the system is in equilibrium before plotting or averaging the dynamic behaviour.

Dynamic model of births, deaths and movement between households

We assume that the distribution of household sizes at time t can be described by a vector $h(n, t)$ defining the number of households of size n. Given the limited data on large households, we assume households have sizes 1–6 in our basic model, and assess the impact of increasing the maximum household size in further analysis. We assume that there are four different types of household events that can occur:

Birth in household of size n:	$h(n,\ t+1) = h(n,\ t) - 1$
	$h(n+1, t+1) = h(n+1, t) + 1$
Death in household of size n:	$h(n, t+1) = h(n, t) - 1$
	$h(n-1, t+1) = h(n-1, t) + 1$
One person moves out of a household of size n:	$h(n,\ t+1) = h(n, t) - 1$
	$h(n-1, t+1) = h(n-1, t) + 1$
	$h(1, t+1) = h(1, t) + 1$
One person moves in to a household of size n:	$h(n, t+1) = h(n, t) - 1$
	$h(n+1, t+1) = h(n+1, t) + 1$
	$h(1, t+1) = h(1, t) - 1$

For simplicity, we assume that an individual moving out of a household enters a household of size one (initially), although this can then be followed by movement into a larger household at the next time-step. Each of the above events occur at a fixed rate per household size. For example, the equations governing deaths in households of sizes 2–6 are:

$$h(n, t+1) = h(n, t) - d(n) * h(n, t) + d(n+1) * h(n+1, t)$$

where $d(n)$ is the death rate in households of size n. We assume that the number of births and deaths balance over the course of a year so the total population size stays fixed. Similarly, we assume that movements into and out of households cancel so that the proportions of households of each type stays constant. This places some constraints on the birth, death and movement rates, but we still need to make some parameter assumptions. For our initial analysis, we use Australian data on birth rates, death rates and movement rates from the Australian Institute of Health and Welfare (Dunn et al., 2002) and the 2001 census from the Australian Bureau of Statistics (ABS, 2008, 2009a,b, 2010). In many cases, demographic parameters are closely related to age, which in turn is associated with household size. As our model does not include age structure, we have attempted to adjust household parameters according to known age-specific patterns. Where specific data are not available, we make assumptions as described below. In order to test these assumptions, we also outline alternative parameter values used for comparison. In performing these comparisons, we maintain a fixed population size and distribution of households so that the model can reach an equilibrium, and so that the impact of parameter values can be distinguished from population changes. In order to maintain fixed population statistics, it is necessary to change sets of parameters at as time, as outlined below.

Death rates

We were not able to obtain data on death rates by household size for Australia. We approximate these by stratifying the population into those aged 75 and over and those under 75, assuming that individuals aged 75 or over have a death rate d_1 and all others have a death rate d_2. Death rates increase exponentially with age (see ABS, 2009b), and we approximate these data by setting $d_1 = 15d_2$. Older people are most likely to live in couple-only families or alone, and so we assume households of size 3 or greater have no individuals over the age of 75. The fraction of one-person households that contain an individual aged 75 or older is approximately 0.22, while around 9% of adults in two-person households are 75 or over. Thus, we assume that the death rate for households of size one is $0.22d_1 + 0.78d_2$, the death rate for households of size two is $2(0.09d_1 + 0.91d_2)$, and death rates for households of size $n = 3, \ldots, 6$ are nd_2.

Alternative death rates considered for comparison include:

- All individuals equally likely to die: $d(n) = nd_0$.
- At most two household members at risk of death: $d = (1, 2, 2, 2, 2, 2)d_0$.
- Every household equally likely to have a death: $d(n) = d_0$.

For each of these four assumptions the final parameter is calibrated to fit population birth and death rates of 0.0135 deaths per population per year (UN, 2007), assuming a fixed population size.

Birth rates

Again, we were not able to find data on birth rates by household size, and so use data on numbers of children born to women between the ages of 20 and 40 (in five year age groups) to approximate a birth rate vector, assuming that 97% of births occur to households with two parents (ABS, 2009a). We assume an overall birth (and death) rate for the population of 0.0135 births per population per year (UN, 2007). This gives us a birth rate vector of $b = (0.002, 0.041, 0.075, 0.038, 0.032, 0)$, where $b(n)$ is the fraction of households of size n that have a birth per year, assuming that all births occur in households of sizes 1–5 (that is, the birth rate in households of size six is zero). A larger maximum household size is also considered in the international comparison described below.

Alternative birth rates considered for comparison include:

- Every household equally likely to have a birth: $b = b_0$, $n = 1, \ldots, 5$.
- Higher birth rate in larger households: $b = (0.023, 0.023, 0.055, 0.055, 0.055, 0)$.
- Higher birth rate in small households: $b = (0.025, 0.04, 0.05, 0.035, 0.025, 0)$.

Household movement rates

Most children move out of home between the ages of 18 and 25, while the median duration of marriages ending in divorce in Australia is about 12 years. This suggests that a child moves out of the household with probability 0.04–0.05 per year. Adult behaviour is more complicated, since only one individual leaves the household in the event of divorce, single parents rarely leave a household, and many marriages do not end in divorce. For simplicity, we assume that adults also move out of a household with probability 0.04, thus making the probability that an individual leaves a household proportional to the household size, that is we have $out = (0, 0.04, 0.08, 0.12, 0.16, 0.20)$.

Alternative movement rates considered for comparison include:

- Everyone equally likely to leave a household: *out* = (0, 0.05, 0.08, 0.11, 0.13, 0.16).
- More departures from large households: *out* = (0, 0.03, 0.08, 0.13, 0.18, 0.23).
- More departures from small households: *out* = (0, 0.05, 0.08, 0.11, 0.14, 0.17).

As a consequence of the assumption that the proportion of households of each type stays constant over time, the rates of movement into the household are fixed once the births, deaths and movement rate out of the household have been specified. For the default rates, this gives us *in* = (0.11, 0.01, 0.08, 0.06, 0.06, 0).

Static model

In order to investigate the effect of including movement between households, we compare our dynamic model to a simple static household model. If we simulated an entirely static model with no births, the model would show a single outbreak and then the disease would die out. This is not informative for assessing immunity by household size at equilibrium. Instead, we include births and deaths (but not movement between households) without changing the household structure simply by setting a proportion 0.0135 of the population to be susceptible over the course of a year. That is, we assume a fraction of individuals die and are replaced in their household by a susceptible. We select individuals at random, although for computational simplicity, we assume that no more than one individual is set to susceptible per household per generation. Individuals are not selected according to their immune status, so in some cases the transition corresponds to replacing a susceptible with a susceptible – in other words, doing nothing.

International comparison

The default model is based on Australian data. Given the much greater model sensitivity to birth rates than any other parameter, we estimate birth rate vectors for a range of countries for comparison with the default model, maintaining the same death and movement rates. Although these death and movement rates are likely to be somewhat inaccurate for developing countries, the model is remarkably insensitive to these parameters, making the choice of values of relatively little importance. We used data from several United Nations (UN) demographic yearbooks to parameterize births and household distributions. The 2007 yearbook was used to select the crude birth rate, the 1995 yearbook (which has a special topic on households) to determine the distribution of household sizes, and a special census topic on number of children born to women by age to estimate a birth rate vector (UN, 1995, 2006, 2007). Since some of these countries have a much larger mean household size than Australia, we also extended our model to allow for a maximum household size of 10. Countries with a mean household size of 3 or greater were only included if there were sufficient data to parameterise this extended model. That is, countries were included if they had data for each of the crude birth rate, the household distributions and the number of children born to women by age group for households of sizes 1–6 if the mean household size is less than 3, and for households of sizes 1–10 if the mean household size is greater than 3. We also restricted our study to countries with population of at least 2 million, to ensure that the disease could be maintained in the population without importations. The 12 countries included in the analysis are shown in Table 1.

We found very limited international data on the number of adults in households where births occur. Although data on illegitimacy is often collected, this seemed likely to greatly overestimate the number of single-parent births in some countries. We adopted the Australian estimate of 3% of births occurring to a single mother (ABS, 2009a). We also tested the sensitivity of our model to households containing other adults using data on the number of family nuclei in household data from the UN yearbooks where this was available (see Table 1). For example, data for the Republic of Korea show that 6.6% of households contained more than one family nucleus, while in Panama, 12.7% of households contained multiple nuclei.

Results

In Fig. 1, we compare case numbers and immunity by household size over time in the household model with and without dynamic transitions. The model shows an approximately biennial outbreak cycle in both the static and the dynamic model, which is reflected by fluctuations in immunity by household size. Where the models differ is in the pattern of immunity by household size. In the static model, the levels of immunity are relatively similar across household sizes, with highest immunity in the larger households. In comparison, there is a wide range of levels of immunity in the dynamic model, with highest immunity in households of size one or two, and lowest immunity in three-person households. Note that we have adopted a different scale to plot immunity for the two models in order to make all curves easily visible. This scale makes it appear as though oscillations are greater in the static model, however they are in fact comparable.

In the dynamic model of Fig. 1, we used the default assumptions for birth rates, death rates and movement of individuals between households. In order to test the sensitivity of our results to these assumptions, we run a series of simulations in which we consider alternative assumptions for each of these rates in turn, and compare these to the results of the static model. Details of the alternative assumptions are provided in the methods. The results are shown in Fig. 2, where we plot the equilibrium immunity profile by household size for each set of alternative assumptions. In all cases, the simple static model produces very different results from the dynamic model. Within the dynamics model, we see that varying the assumptions concerning death rates or movement between households has very little impact on patterns of immunity by household size. In contrast, changing the pattern of births can change the immunity profile considerably. This suggests that it is the movement of susceptible individuals that is the primary driver of household immunity in our dynamic model. We tested the impact of the disease-specific parameters on these results by considering alternative values of μ and θ. Although the overall level of immunity is different with these disease parameters, we found that the relative pattern of immunity by household size was very similar (results not shown).

In addition to the pattern of immunity by household size, we are also interested in the risk of infection by individual and by household. Table 2 presents details of the model population of households of sizes 1–6 under the default demographic assumptions, together with statistics of the simulation model of infection. The table presents the proportion of individuals immune, cases per 1000 individuals and cases per 1000 households by household size. One and two person households have the highest immunity and the lowest risk of infection – largely because most one and two person households do not contain children, and we are considering a disease that confers life-long immunity. The risk of infection per household is greatest in the largest households, but the risk of infection per individual is highest in three and four person households – that is, the households that are most likely to have recently had a birth.

Table 1
List of population sizes, birth rates and mean household sizes for countries considered in the dynamic model.

Country	Population	Birth rate[a]	Mean household size	Proportion of households with multiple nuclei[b]
Australia	19,143,800	13.5	2.6	
Canada	24,773,105	10.7	2.7	
China	1,097,776,366	12.0	4.0	
Egypt	47,995,265	26.5	4.9	
Finland	7,839,697	11.1	2.6	
Hungary	10,123,829	9.7	2.6	
Korea	39,121,522	10.3	4.1	0.066
New Zealand	3,095,406	15.1	2.9	0.033
Panama	2,307,306	20.2	4.4	0.127
Romania	22,385,707	10.0	3.1	0.062
Russia	147,021,869	11.3	2.6	
Turkey	50,813,802	17.3	5.2	

[a] Annual births per 1000 individuals.
[b] Where this statistic is available.

Our default assumptions are derived from Australian census data. Australia is typical of western countries in having a relatively low birth rate and an average household size of less than 3. Countries with different demographic characteristics might be expected to show different patterns of infection by household size. Table 1 shows a list of 12 countries with data on population size, mean household size and birth rate. These countries were selected as those with sufficient information on fertility and household distributions in the UN Demographic Yearbook (UN, 1995, 2006, 2007) to calibrate birth rates in the dynamic model.

In Fig. 3, we compare the number of cases per 1000 households by household size for the 12 countries listed in Table 1, grouped by mean household size and birth rate. For countries with a high mean household size (3 or greater), we use a model with maximum household size of 10, and for those with a low mean household size (less than 3), we use a model with maximum household size of 6. We also compared model outputs for two countries (New Zealand and Canada) with low mean household size for which there were sufficient data to calibrate the extended model, and confirmed that the model with maximum household size of six is sufficient for these countries. All countries displayed in Fig. 3 show a low risk of infection in households of size one and two, but the pattern in larger households varies according to the mean household size and the birth rate. Countries with a low mean household size (Australia, Canada, Finland, Hungary, New Zealand and Russia) all show a similar pattern of gradually increasing risk of infection with household size. This pattern does not seem to be greatly affected by the variation in birth rate (9.7–15.1 annual births per 1000 individuals) over these countries.

Among countries with a high mean household size of (3 or greater), there is an effect of birth rate. Countries with a *low* birth rate (China, Korea, Romania) show a generally increasing risk of infection with household size, reaching a plateau or slightly dropping for very large households. In contrast, countries with both a *high* birth rate and a large mean household size (Egypt, Turkey, Panama) show the greatest risk per individual in households of sizes 3–5, with relatively low risk in larger households. This observed peak in household-level susceptibility arises because in such populations many 3 and 4 person households have recently experienced a birth, accounting for their relatively high risk of infection. Finally, we also considered the impact of multiple adult residents as a driver of larger household sizes using demographic data on the number of household nuclei for four countries in Fig. 3 with different demographic characteristics (Korea, New Zealand, Panama and Romania). We found that including extra adults in our birth rate calculations resulted in only a slight impact on immunity and risk of infection, and did not change the broad patterns shown in Fig. 3.

Discussion

Households play a key role in transmission of infectious diseases. While many infectious disease models include households, they typically assume a static household distribution and do not include births, deaths and movements in and out of the family unit. This is a reasonable simplification for assessing current risks and for predicting disease patterns over the short (weeks-months) time scale of a typical infectious disease outbreak, but has clear limitations for understanding and predicting medium- to long-term patterns of infection and immunity. This paper introduces a household transmission model that includes demographic changes. We show that different assumptions concerning movement patterns among households can change infection patterns considerably, and that these patterns also vary according to the distribution of household sizes.

The simplest demographic assumptions for a household transmission model are that births and deaths occur evenly across households. These simplistic assumptions lead to low immunity in one- and two-person households and high immunity in large households. When more realistic demographic assumptions are adopted, however, this finding is reversed, with high levels of immunity in smaller households. The results of the realistic model are in agreement with empirical data on households – for example, House and Keeling (2009) found that "over 90% of households of

Table 2
Impact of household size on immunity and risk of infection by household and by individual in a population of 19.1 million individuals across 7.4 million households. The first three columns show characteristics of our model population, the second three columns the infection statistics calculated from model simulations.

Household size	Number of households (millions)	Number of individuals (millions)	Proportion of individuals immune	Cases per 1000 individuals	Cases per 1000 households
1	1.75	1.75	0.96	0.18	0.18
2	2.48	4.96	0.97	0.14	0.27
3	1.23	3.68	0.91	0.49	1.46
4	1.18	4.74	0.92	0.46	1.86
5	0.55	2.77	0.93	0.42	2.08
6	0.21	1.24	0.94	0.38	2.26

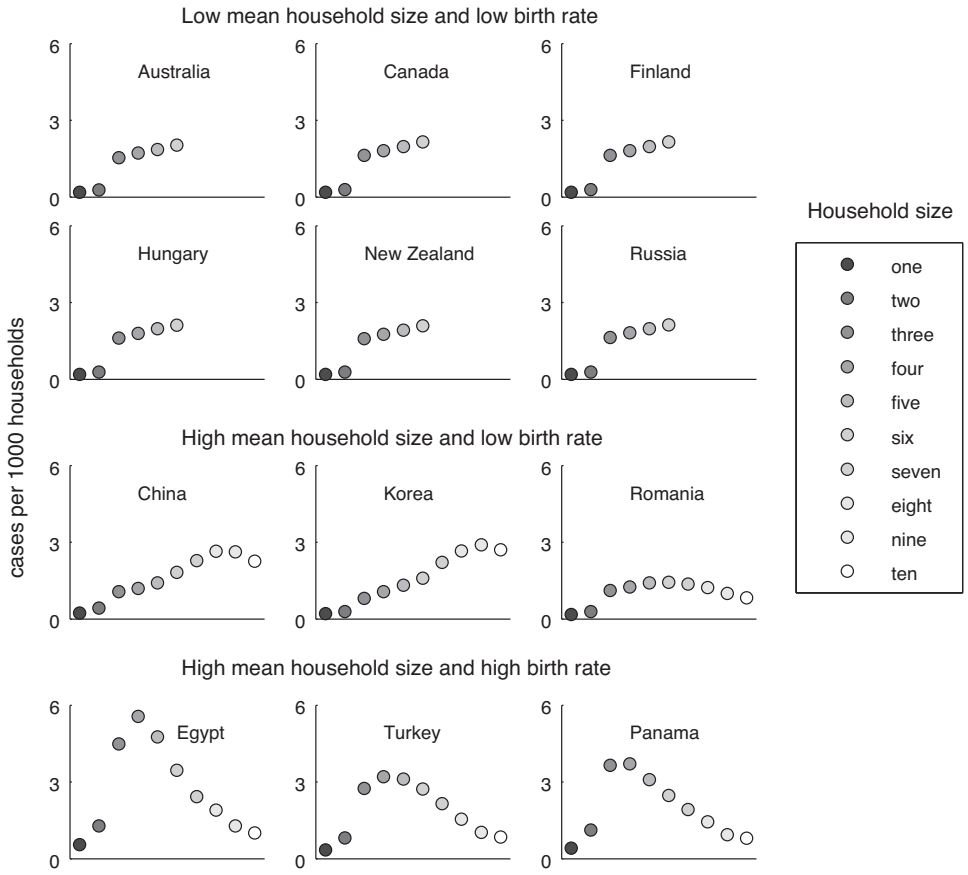

Fig. 3. The number of cases per 1000 households by household size for the 12 countries listed in Table 1, divided according to mean household size and birth rate. The top two rows present results for countries with a low crude birth rate (under 16 births per 1000 individuals) and a low mean household size (less than 3). The third row presents countries with a high mean household size (over 3) and a low birth rate (under 16 births per 1000 individuals). The fourth row presents countries with a high mean household size (over 3) and a high birth rate (over 16 births per 1000 individuals).

size two have no dependent children". It is the larger households, which are more likely to have had recent births, which we expect to contain susceptibles. The sensitivity of the results to demographic assumptions highlights the need for realistic population movement patterns to model infection in households.

An analysis of model parameters identified that births are the main driver of differences in immunity between households of different sizes, with death rates and movement rates having much less impact on equilibrium behaviour. This result remained despite changes to disease-specific parameters, and we believe it is because birth rates determine the influx of susceptibles into the model. It seems plausible that other demographic parameters may become important for diseases such as pertussis, where waning of immunity becomes an important factor in disease transmission (Aguas et al., 2006). One of the difficulties in parameterising our model is in obtaining data on birth rates by household size. In order to derive plausible birth rate parameters, we have imputed birth rates from data on the number of children born to women in 5 year age groups, which we believe provides a reasonable approximation to the true situation.

Our default model is calibrated to Australian data. In an international comparison, we found that both the crude birth rate and the mean household size influence the risk of infection. Countries with few large households show a fairly consistent pattern of high immunity and low risk of infection in one- and two person households, and gradually rising risk of infection in three to six person households. Countries with larger household sizes show differing patterns of infection according to the birth rate. Countries that have both a high birth rate and a large mean household size show the greatest risk per individual in households of sizes 3–6, with declining risk in large households. In contrast, countries with a relatively low birth rate and large household size show greatest risk of infection per individual in households of sizes 6–9.

Although we have not explicitly modelled vaccination, our results have implications for vaccination strategies. Optimal vaccination strategies are likely to vary between countries, and also within countries over time as population ageing and smaller average household sizes change the demographic patterns. It is also likely that optimal vaccination strategies may differ for different household sizes – for instance Melegaro et al. (2004) identified that when considering pneumococcal carriage, transmission within the household is most important in large families.

We believe that the model presented here provides a good first step for understanding the interaction between demographic patterns and disease incidence, however we acknowledge that it is very simple. In particular, we are not able to include age-specific infection and demographic patterns explicitly. In future work, we plan to move to a more extensive individual-based model with households as a primary unit. This project is ambitious, but would give us the scope to incorporate age structure and more realistic mixing patterns outside the household, as well as waning of immunity, the rate of which may be explicitly related to household risk of infection exposure. We aim to develop this more detailed model in stages, with the aim of considering the impact of gradual population changes in age and household structure over time

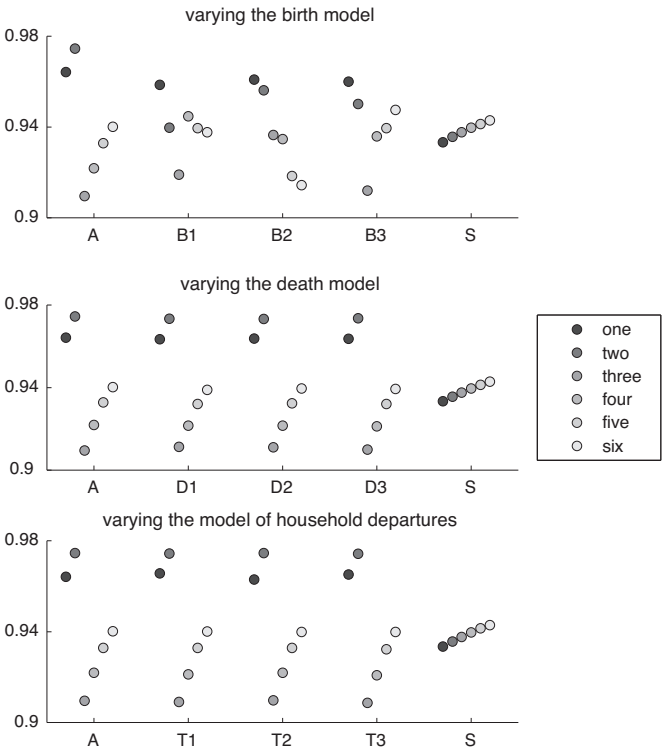

Fig. 2. The effect of changes to parameters governing births (top), deaths (middle) and household departures (bottom) on immunity by household size. Each data point reports the mean value over 100 generations. The models considered are: (A) default model of births, deaths and household departures; (B1) every household equally likely to have a birth; deaths and departures as (A); (B2) higher birth rate in large households; deaths and departures as (A); (B3) higher birth rate in small households; deaths and departures as (A); (D1) all individuals equally likely to die; births and departures as (A); (D2) at most two household members at risk of death; births and departures as (A); (D3) every household equally likely to have a death; births and departures as (A); (T1) everyone equally likely to move out of a household; births and deaths as (A); (T2) more departures from large households; births and deaths as (A); (T3) more departures from small households; births and deaths as (A); (S) static model presented in Fig. 1.

on disease incidence and immunity, as well as the impact of more drastic demographic transitions, such as are observed in rapidly industrializing populations. This body of work will provide a framework allowing more nuanced exploration of the likely medium to long-term impact of interventions to limit disease transmission in diverse populations.

Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at doi:10.1016/j.epidem.2011.05.001.

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